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For: MUTANT B-TYPE POLYMERASES
IMPROVED PERFORMANCE IN PCR

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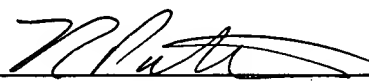
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Mutant B-type DNA polymerases exhibiting improved performance in PCR

FIELD OF THE INVENTION

Subject of the invention is a thermostable mutant B-type DNA-polymerase having a Y-GG/A amino acid motif between the N-terminal 3'-5'-exonuclease domain and the C-terminal polymerase domain in the wild type form whereas amino acids of this motif are substituted in the mutant form of the DNA polymerase and whereas these mutant DNA polymerases are suitable for PCR reactions. Thermostable mutants according to the present invention exhibit better performance in PCR reactions compared to the wild type DNA polymerase. A further embodiment of the present invention is the use of these thermostable mutants of the B-type DNA polymerase for polymerase chain reactions (PCR) and other nucleic acid synthesizing reactions. Another subject of the present invention is a method of producing the inventive mutants, vectors and cell lines comprising genes encoding the inventive mutants.

BACKGROUND OF THE INVENTION

DNA-dependent DNA polymerases containing proof-reading activity have to coordinate two catalytic activities: the DNA polymerase activity and the exonuclease activity. For polymerase I type DNA polymerases (*E. coli* Pol I) as well as for B-type DNA polymerases, these catalytic activities are located on structurally distinct protein domains (Truniger, V., Lázaro, J., Salas, M. and Blanco, L. (1996) *EMBO J.*, 15(13), 3430-3441; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). In B-type (eukaryotic-type) DNA polymerases, the coordination of the two catalytic activities was proposed to take place intramolecularly in the conserved motif Y-GG/A located between the N-terminal 3'-5' exonuclease and the C-terminal polymerization domain (Truniger, V., Lázaro, J., Salas, M. and Blanco, L. (1996) *EMBO J.*, 15(13), 3430-3441; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). For the Klenow fragment of *E. coli* DNA polymerase it was described, that the editing can

be an intermolecular or intramolecular process involving dissociation and reassociation of the DNA depending on the local context (Joyce, C. M. (1989) *JBC*, 264(18), 10858-10866). Truniger et al. (Truniger, V., Lázaro, J., Salas, M. and Blanco, L. (1996) *EMBO J.*, 15(13), 3430-3441) demonstrated for the mesophile replicative DNA polymerase of bacteriophage ϕ 29 that mutations in the Y-GG/A motif can lead to phenotypes favoring either polymerisation or exonucleolysis compared to the wild type enzyme. They could show that this effect is related to altered (ss)DNA binding parameters and that the motif is important for the communication between the polymerase and exonuclease active site in a combination of structural and functional roles.

For the DNA polymerase of the thermophilic crenarchaeon *Sulfolobus solfataricus* (*Sso*) a region of 70 amino acids (region 1) involved in enzyme-DNA interaction was determined (Pisani, F. M., Manco, G., Carratore, V. and Rossi, M. (1996) *Biochemistry*, 35, 9158-9166). It is located in the connecting part between the exonuclease domain and the polymerase domain and contains the Y-GG/A motif. By mutational analysis of the amino acids in the Y-GG/A motif, it could be shown that the amino acids in this part of the enzyme determine the processivity of the proofreading function (Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). Based on the crystal structure of bacteriophage RB69 DNA polymerase, Truniger et al. proposed a direct interaction of the tyrosine with the phosphodiester bond between the two nucleotides preceding the one acting as template (Truniger, V., Blanco, L. and Salas, M. (1999) *J. Mol. Biol.*, 286, 57-69).

DESCRIPTION OF THE INVENTION

The subject of the present invention was to provide thermostable DNA polymerases exhibiting an improved performance in PCR. Especially, thermostable mutants of a B-type DNA polymerase are provided which exhibit improved PCR performance. The inventive mutants of the B-type DNA polymerase have mutations in the Y-GG/A amino acid motif. Preferred mutations refer to the position of the tyrosine in the Y-GG/A amino acid motif. Other mutations affecting the motif could also influence the performance of B-type DNA polymerases in PCR.

According to the present invention an improved performance of a DNA polymerase in PCR is defined as a performance that results in higher yields of PCR product, or the amplification of

longer DNA targets. Additionally, improved PCR performance can be defined as improved fidelity during the amplification process.

Preferred mutant B-type DNA polymerases have mutations at the position of the tyrosine in the Y-GG/A amino acid motif. Preferred mutants of B-type DNA polymerases according to the present invention have phenylalanine, tryptophan or histidine at the position of the tyrosine. Other preferred mutants of B-type DNA polymerases according to the present invention have asparagine or serine at the position of the tyrosine. These mutant polymerases described here, in which the tyrosine of the Y-GG/A motif was substituted, exhibit an improved performance in PCR.

In a preferred embodiment the inventive mutant B-type DNA polymerase is a mutant of a B-type DNA polymerase obtainable from Euryarchaea, more preferably from *Thermococcus aggregans* (Tag). Especially preferred is a mutant of a B-type DNA polymerase from Tag of about 94 kDa size with a temperature optimum of $\geq 80^{\circ}\text{C}$ and the ability to perform polymerase chain reactions.

The present invention is described in detail for the B-type DNA polymerase from *Thermococcus aggregans*, but the invention could also be applied to other B-type DNA polymerases. Preferably to those B-type DNA polymerases showing a high degree of homology ($\geq 80\%$) to the DNA polymerase from *Thermococcus aggregans*.

The B-type DNA polymerase from *Thermococcus aggregans* exhibits a high degree of amino acid sequence homology to B-type DNA polymerases of other *Thermococcus* species. The homology of the DNA polymerases was calculated using the program Blast 2 (Tatusova, T.A. and Madden, T.L. (1999) *FEMS Microbiol. Lett.* 174, 247 – 250). The homology of the B-type DNA polymerase from *Thermococcus aggregans* to the homologue enzymes from *Thermococcus* species is: 93% (*T. litoralis*), 87% (*T. gorgonarius*), 86% (*T. furiosus*) and 87% (*T. spec.* 9N7). The homology of the Tag DNA polymerase to polymerases from *Pyrococcus* species is: 86% (*P. abyssii*), 86% (*P. horikoshii*), 86% (*P. spec* KOD) and 85% (*P. furiosus*). A lower homology is calculated to other B-type DNA polymerase from different euryarchaeota: 59% (*Methanococcus jannaschii*), 56% (*Methanococcus voltae*), 51% (*Methanobacterium thermoautotrophicum*) and 56% (*Archaeoglobus fulgidus*). To B-type DNA polymerases from crenarchaeota and bacteriophages the homology is found as follows: 46% (*Sulfolobus solfataricus*), 42% (*Sulfolobus acidocaldarius*), 41% (*Sulfurisphaera ohwakuensis*), 51% (*Aeropyrum pernix*), 40% (*Pyrodictium occultum*), 43% (*Cenarchaeum symbiosum*), 38% (bacteriophage T4) and 39% (bacteriophage RB69).

As described above several mutations in the Y-GG/A motif were performed for the *Sulfolobus solfataricus* (*Sso*) and the ϕ 29 DNA polymerases. The observed effects on polymerase activity (pol) and exonuclease activity (exo) of these mutations do not completely correspond to the effects obtained for the *Tag* DNA polymerase. Thus the effect of the mutations on the performance of the mutants in PCR was not predictable.

The mutant Y387F of the *Tag* DNA polymerase exhibits a higher pol/exo ratio compared to the wild type *Tag* DNA polymerase. Similar results were described for *Sso* and ϕ 29 DNA polymerase. The mutant G389A displays the opposite effect than the corresponding mutant in ϕ 29 DNA polymerase: while G→A in *Tag* DNA polymerase almost knocks out polymerase activity, in ϕ 29 DNA polymerase G→A mutant this activity is clearly enhanced. For mutants of the *Sso* DNA polymerase a change of exonuclease processivity was described. Again, this was not observed for mutants of the B-type *Tag* DNA polymerases. Thus, a prediction of the effect of analogous mutants in the Y-GG/A motif could not be made.

In summary, although it has been described in the prior art that the Y-GG/A motif plays a role in the coordination of the DNA polymerase activity and the exonuclease activity, the observed changes of the pol/exo ratio of the prior art DNA polymerases do not strictly correlate to the changes observed for the inventive mutants of the *Tag* DNA polymerase. Furthermore, it has not been described that the Y-GG/A motif is important for the performance of B-type DNA polymerase in PCR. Additionally, there is no correlation between the changes of the pol/exo ratio and the improvement of the performance of DNA polymerases in PCR. For instance, the mutant Y387H does not exhibit a change of pol/exo ratio compared to the wild-type, but it exhibits improved performance in PCR. Furthermore, a significant enhancement of fidelity was observed for the mutants Y387N and Y387S of *Tag* DNA polymerase.

Results obtained for the mutants of *Tag* DNA polymerase are described in more detail below.

Enzymatic activities of wild type and mutant *Tag* DNA polymerases

The enzymatic activities of the wild type enzyme and the mutants of *Tag* DNA polymerase were determined and analyzed (Figure 1). The DNA polymerase activity was determined as described in Example 2. According to the effect of the mutations on the polymerase activity three groups of

mutants were defined: i) mutants with enhanced DNA polymerase activity (mutant Y387F), ii) mutants having a similar or slightly reduced DNA polymerase activity compared to the wild type (mutants Y387W and Y387H) and iii) mutants with reduced DNA polymerase activity (mutants Y387N, Y387S, G389A).

The exonuclease activity was determined as described in Example 3. According to the effect of the mutations on the exonuclease activity two groups of mutants were defined: i) mutants with similar exonucleolytic activity as the wild type enzyme (mutants Y387F, Y387W, Y387H), ii) mutants with enhanced exonuclease activity (mutants Y387N, Y387S, G389A) in comparison to the wild type enzyme.

From the data obtained for polymerase activity and exonuclease activity the ratios of both activities (pol/exo) were calculated for the wild type enzyme and the mutants of *Taq* DNA polymerase (Figure 1). Three mutants showed a higher or similar pol/exo ratio as the wild type enzyme (mutants Y387F, Y387W, Y387H). Three mutants showed a clearly reduced pol/exo ratio in comparison to the wild type enzyme (mutants Y387N, Y387S, G389A).

PCR performance

Wild type and mutant enzymes were submitted to polymerase chain reactions on lambda DNA in a buffer optimized for this purpose. All mutants except for mutant G389A were able to perform PCR, but yielded different amounts of product with a constant amount of enzyme (1 pmol). With increasing length of the DNA target, differences in performance of the enzyme were shown (Fig. 2). With 1 pmol of the mutants Y387S, Y387N and G389A no PCR product could be obtained for the amplification of a 3.3 kb fragment. 1 pmol of the wild type DNA polymerase could not amplify fragments of 5.0 kb length. The mutants Y387W, Y387F and Y387H were able to amplify a fragment of 7.5 kb length. As control *Taq* DNA polymerase, *Pwo* DNA polymerase and ExpandTM High Fidelity PCR System (Roche Molecular Biochemicals) were used.

The differences in PCR performance were also shown by the amplification of a 2 kb fragment applying different elongation times in the PCR runs. Under these conditions, all enzymes tested except the mutant G389A were able to amplify a 2 kb fragment at an elongation time of 90 sec/cycle. The mutants Y387F, Y387W and Y387H were able to amplify the fragment at a reduced elongation time of 40 sec/cycle. The mutant Y387H was able to amplify the target in a elongation time of 30 sec/cycle (Fig. 3).

Exonuclease processivity

The exonuclease processivity of the enzymes was studied in an experiment based on the heparin trap method (Reddy, M. K., Weitzel, S. E. and von Hippel, P. H. (1992) *J. Biol. Chem.*, 267(20), 14157-14166; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). A constant amount (1 pmol) of *Tag* DNA polymerase or its mutants was incubated for 4 minutes at 68 °C with a 5'-DIG-labelled 24mer oligonucleotide in the absence of nucleotides. In the absence of heparin, the oligonucleotide was continually degraded by the *Tag* enzymes (positive control, Fig. 4, lanes "-"). The function of the heparin trap method was demonstrated by addition of heparin and $MnCl_2$ before the binding of the enzyme (negative control, Figure 4, lanes B). Single turnover conditions (addition of heparin and $MnCl_2$ to start the reaction after the binding of enzyme) resulted in exonucleolytic degradation of the oligonucleotide by the *Tag* DNA polymerases (Fig. 4, lanes A). The enzymes showed differences in the exonucleolytic activity as shown by the different amounts of remaining oligonucleotide that was not degraded. However, for all enzymes tested the oligonucleotide was degraded to a similar extent (8 nt). This indicates a similar exonuclease processivity for the enzymes.

The *Thermococcus gorgonarius* DNA polymerase, which exhibits a strong exonuclease activity, was used as a positive control. It degraded the 24mer oligonucleotide in the absence of heparin to oligonucleotides of less than 15 bases length (Figure 4, lane "-"). Under single turnover conditions a strong degradation (11 nt) of the oligonucleotide is observed (Figure 4, lane "A").

Fidelity

The error rates in amplification were determined for the mutant enzymes and the wild type DNA polymerase. The PCR-based fidelity assay described by Frey and Suppmann (Frey, M. and Suppmann, B. (1995) *Biochemica*, 2, 34-35) was used. This method is based on the amplification, circulation and transformation of the pUC19 derivative pUCQ17, which contains a functional *lacI^q* allele (Barnes, W. M. (1994) *Proc. Natl. Acad. Sci. USA*, 91, 2216-2220). PCR-derived mutations in *lacI* result in a de-repression of the expression of *lacZ α* and subsequent formation of a functional β -galactosidase enzyme, which can be detected on X-Gal indicator plates.

In five independent runs, a mean error rate of 5.0×10^{-6} was found for the wild type *Tag* DNA polymerase. This value is in between the mean error rates of 1.8×10^{-6} for ExpandTMHigh Fidelity PCR System (Roche Molecular Biochemicals) and 1.3×10^{-5} for *Taq* DNA polymerase

(Roche Molecular Biochemicals) determined in the corresponding experiments. For a better comparison of the data, we plotted the quotient of the error rate determined for *Taq* DNA polymerase divided by the error rates determined for the *Tag* DNA polymerase and its mutants. In the independent experiments the error rate for *Taq* DNA polymerase varied from 1.2 to 3.05×10^{-5} .

Figure 5 shows the quotients of the error rates of the wild type enzyme and mutants of *Tag* DNA polymerase. The error rates of the mutants showing improved PCR performance (Y387W, Y387F, Y387H) did not significantly differ from the values obtained for the wild type enzyme. The mutants with enhanced exonuclease activity (Y387N, Y387S) showed improved fidelity rates (Figure 5). For the mutants Y387N and Y387S mean error rates of 6.3×10^{-7} and 6.2×10^{-7} were determined.

In contrast to the $\phi 29$ DNA polymerase and the *Sso* DNA polymerase, the *Tag* DNA polymerase, is suited for PCR. The mutant enzymes (Y387F, Y387W, Y387H) with an aromatic amino acid in the position of the tyrosine showed a similar or only slightly enhanced DNA polymerase activity (mutants Y387F, Y387W, Y387H) but an improvement in PCR performance.

In the fidelity assay it was found that the mutants Y387F; Y387W and Y387H showed no significant change in their error rate. By contrast, the mutants Y387N or Y387S showed higher exonuclease activity and displayed an improved fidelity.

Subject of the present invention is also a method of producing the inventive B-type mutants comprising the following steps: cloning and mutagenesis of the gene, followed by the expression and purification of the protein.

Subject of the present invention is a DNA encoding for a thermostable B-type DNA polymerase having a Y-GG/A amino acid motif between the N-terminal 3'-5' exonuclease domain and the C-terminal polymerase domain in the wild type enzyme whereas the tyrosine of this motif is substituted in the mutant enzyme of the polymerase and whereas this mutant DNA polymerase is suitable for PCR.

Preferably, said DNA in wild type form is obtainable from Euryarchaea, more preferably from *Thermococcus aggregans* (*Tag*). Subject of the present invention is also a vector containing the inventive DNA. Suitable vectors are e.g. the following: pET14b/15b/16b/19b (Novagen); pRSET

(Invitrogen); pTrcHis (Invitrogen); pHAT10/11/12 (Clontech); pPRO Tet.E/Lar.A (Clontech); pCALn/n-EK (Stratagene); pGEMEX-1/-2 (Promega).

Furthermore, subjects of the present invention are also cells comprising the above vector. Suitable cells are e.g. *E.coli* BL21, BL21(DE3), BL21(DE3)pLysS, BL21(DE3)pLysE, DH5 α PRO, JM109 (DE3), TOP10 in combination with the vectors recommended by the suppliers. The gene may have to be subcloned and the protein purification procedure may have to be adapted in the case of different expression vectors.

A sample of the recombinant strain expressing *Tag* DNA polymerase was deposited with the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) Mascheroder Weg 1b, D-38124 Braunschweig (DSM No. 13224).

A further subject of the invention is the use of the inventive mutant enzymes for synthesizing nucleic acids e.g. in PCR reactions.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS EPO - Munich
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Figures:**Figure 1.**

Table showing the relative polymerase activities (Pol) and 3'-5'-exonuclease activities (Exo) of *Tag* DNA polymerase and its mutants on double-stranded DNA.

Assays were carried out as described in example 2 and 3, respectively. The activities are expressed as percentage of the activity obtained for the wild-type *Tag* DNA polymerase.

Figure 2.

PCR with *Tag* DNA polymerase mutants.

Tag DNA polymerase mutants (1 pmol) were incubated in a 50 µl total volume with 10 ng of lambda DNA as template and 30 pmoles of a primer set designed to yield the indicated fragment lengths, 200 µM dNTPs and the suitable PCR buffer. Reactions were performed with 10 cycles of 10 sec 94 °C, 30 sec 57 °C and 3.0 min (A), 4.3 min (B) or 7.0 (C) min of elongation time at 72 °C followed by 20 cycles with elongation times increasing by 20 sec/cycle. After the PCR 5 µl sample were submitted to electrophoresis on a 1% agarose gel. For the control reaction 2.5 U of *Taq* DNA polymerase, *Pwo* DNA polymerase or Expand™ High Fidelity PCR System were used. The labeling of the lanes is described in the legend of figure 6.

Figure 3.

Time-dependent polymerase chain reaction.

1% agarose gels showing 2 kb PCR products from reactions performed with different elongation time (90 sec, 40 sec, 30 sec as indicated) to determine the minimal elongation time.

1 pmol of each *Tag* DNA polymerase mutant or wild type enzyme was added to a mix of 10 ng lambda DNA and primers designed to yield 2 kb DNA fragments. Labeling of the lanes is described in the legend of figure 6. For each mutant duplicate reactions were performed. Right lane of each gel *Pwo*: 2.5 U *Pyrococcus woesei* DNA polymerase (Roche Molecular Biochemicals) as control reaction. Left lane of each gel: Molecular weight marker VI (Roche Molecular Biochemicals). In the 40 sec reaction, mutant GA was omitted. In the 30 sec reaction, for the mutant YS only one reaction was run on the gel.

Figure 4.

3'-5'-exonuclease processivity.

The *Tag* DNA polymerase mutants tested are indicated on top of the figure. *Tgo* DNA polymerase was used as a control reaction (incubation for 30 sec). Reactions for wild type and mutants of *Tag* DNA polymerase were performed for 4 minutes at 68 °C after preincubation for 1 minute at 68°C. Lane "P" is the control reaction (24 mer 5'-DIG-labelled primer without incubation), lane "-": reaction without heparin (positive control); lane "B": reaction with heparin and MnCl₂ added before addition of the enzyme (negative control); lane "A": heparin and MnCl₂ added after the enzyme (reaction under single turnover conditions).

Figure 5.

Fidelity of *Tag* DNA polymerase mutants.

The fidelity of *Tag* DNA polymerase and its mutants was expressed in relation to the fidelity of *Taq* DNA polymerase. A quotient of 1 means that the polymerase has the same error rate as *Taq* DNA polymerase (mean value 1.3×10^{-5}). Values >1 reflect the factor by which a polymerase shows less errors than *Taq* DNA polymerase. The bars correspond to mean values calculated from 2-5 independent experiments, error bars missing are smaller than 0.36. Abbreviations for enzymes are as indicated in legend to figure 6. As controls *Pyrococcus woesei* DNA polymerase (Roche Molecular Biochemicals) and Expand High Fidelity PCR System (Roche Molecular Biochemicals) were used („Taq/Pwo“ and „Taq/HiFi“).

Figure 6.

SDS-PAGE gel analysis of purified mutant proteins.

1 µg of each mutant was submitted to electrophoresis on an 10% SDS-PAGE gel. Left: MW, molecular weight marker; WT, *Thermococcus aggregans* wild type DNA polymerase; YF, YW, YS, YN, YH are the corresponding mutants with an exchange at the position of tyrosine 387 to phenylalanine, tryptophan, serine, asparagine, histidine, respectively. GA, mutation of glycine 389 to alanine in the gene of the *Thermococcus aggregans* DNA polymerase. All mutants showed the same chromatographic behaviour and solubility as the wild type enzyme.

Figure 7.**Qualitative exonuclease assay.**

A DNA molecular weight marker was used as substrate to test the exonucleolytic activity (DNA molecular weight marker II (MW II), Roche Molecular Biochemicals). 1 µg of MW II was incubated for 6 h at 65 °C with 1 pmol of each variant of *Tag* DNA polymerase in the presence (A) or absence (B) of 200 µM dNTP. *Tag* mutants are named as explained in legend of figure 6. Exonucleolytic degradation take place only in the absence of deoxynucleotides. The qualitative ranking of the proteins in terms of exonuclease activity is GA > YN > YS > YH > YF = YW = WT.

Figure 8.

Consensus sequence motif for B-type DNA polymerases from the order of *Thermococcales* derived from a multiple alignment of amino acid sequences of euryarchaeal and crenarchaeal B-type DNA polymerases.

A region of 24 amino acids containing the Y-GG/A motif was analyzed with the ClustalW Software program (Higgins, EMBL Heidelberg, Germany). In addition to the amino acids conserved in all archaeal B-type DNA polymerases (like the Y-GG/A motif), a consensus sequence "E--RR-R-----G(Y)-KE-EE--LWE-" can be defined. This sequence is found in the sequence of all DNA polymerases belonging to the order of the *Thermococcales* and coincides with a homology of >80% of the DNA polymerases.

The sequences of the crenarchaeal species *Sulfolobus solfataricus*, *Sulfolobus acidocaldarius*, *Pyrobaculum islandicum*, *Pyrodictium occultum*, *Aeropyrum pernix*, *Sulfurisphaera ohwakuensis* and the sequences of several euryarchaeal species *Thermococcus* ("T."), *Pyrococcus* ("P.") and *Methanococcus* ("M.") were aligned.

Figure 9.

DNA sequence and deduced amino acid sequence of recombinant wild type *Tag* DNA polymerase.

Three inteins found in the native gene (Acc. No. Y13030) were deleted by PCR (Niehaus, F., Frey, B., Antranikian, A. (1997) *Gene*, 204, 153-158). Four mutations leading to amino acid exchanges were introduced during PCR. The amino acid exchanges (native→recombinant) are: L3F, A404T, S410C and L492H.

Example 1

Site-directed mutagenesis and expression of *Tag* DNA polymerase mutants

The cloning of the gene of *Tag* DNA Polymerase (polTY) was described earlier (Niehaus, F., Frey, B., Antranikian, A. (1997) *Gene*, 204, 153-158). Overexpression of *Tag* DNA Polymerase in *E. coli* was achieved by subcloning its encoding gene into the IPTG-inducible pET15b vector (Novagen) containing an N-terminal His-Tag for purification (the resulting plasmid was named pET15b-TagPol).

The mutants presented in this study were prepared in polymerase chain reactions using primers containing the desired mutations as a mismatch. The forward primer was universally "Kpn-fw", matching to a sequence about 100 bp upstream of the mutation site and contained a *KpnI* restriction site of the polTy gene. The reverse primers contained a *SnaBI* restriction site and additionally the desired mutation. The sequences of the oligonucleotides were as follows (mismatch sites for mutagenesis underlined):

Kpn-Fw 5'-GCAACCTTGTAGAGTAGAGTGGTACCTGTTAAGGG-3';
TagY387F 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGAAAGTAGTCC-3',
TagY387H 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGTGAGTAGTCC-3',
TagY387N 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGTTAGTAGTCC-3',
TagY387S 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGGAAGTAGTCC-3',
TagY387W 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGCCAAGTAGTCC-3',
TagG389A 5'-GCCTCTTTCCGGCTCTTTTACGTATCCAGCCAGGTAAGTAGTCC-3'.

PCR reactions were carried out with ExpandTM High Fidelity PCR System (Roche Molecular Biochemicals) using the following program: 2 min 94 °C, 30 cycles of 10 sec 94 °C, 30 sec 55 °C, 30 sec at 72 °C. The resulting 139 bp fragments were digested with the restriction enzymes *KpnI* and *SnaBI* yielding a 101 bp fragment that was ligated into pET15b-TagPol linearized with the restriction enzymes *KpnI* and *SnaBI*. The cloned DNA fragments were sequenced to confirm the presence of the desired mutations.

For protein expression, *E. coli* BL21 (DE3) cells were transformed with the expression vector pET15b-TagPol. Three to five colonies were inoculated in 15 ml of LB medium supplemented with 100 µg Ampicillin per ml and grown to OD_{600nm} 0.3. An aliquot (10 ml) of the preculture was used to inoculate 500 ml of LB medium and incubated while shaking at 37°C. At OD_{600nm} = 0.6 expression was induced by addition of IPTG (final concentration: 1 mM). After incubation

for 3 hours cells were harvested by centrifugation and suspended in 50 mM Tris-HCl/pH 7.5, 10 mM KCl, 0.5 mM EDTA, 4 mM MgCl₂, 5 mM DTT. Cells were sonicated on ice and the crude extract was heated for 15 min to 80 °C. Cell debris was removed by centrifugation (30 min, 30 000 x g at 4 °C).

The supernatant was applied to a Blue Sepharose 3G-A column (Pharmacia) equilibrated with buffer A (50 mM Tris-HCl/ pH 7.5, 10 mM KCl, 4 mM Mg Cl₂). The protein was eluted with a gradient of 0.01-1.5 M KCl. Active fractions were pooled and dialyzed against 20 mM Tris-HCl /pH 7.9, 5 mM imidazole, 500 mM NaCl. The sample was applied to a Ni-chelate column (Novagene) equilibrated in the same buffer and eluted with a gradient of 0.005 - 1 M imidazole. Active fractions were pooled and dialyzed against storage buffer (50 mM Tris-HCl/pH 7.5, 100 mM KCl, 0.5 mM EDTA, 5 mM DTT, 50% glycerol). The enzymes were pure as shown by SDS gel electrophoresis (Figure 6).

Example 2

DNA polymerase assay

The DNA polymerase activity was determined by measuring the incorporation of α -(³²P)dCTP in a DNA substrate. The test mix (50 μ l) contained 5 μ l 10x Tag reaction buffer (100 mM Tris-HCl /pH 8.9, 750 mM KCl, 15 MgCl₂, 100 mM CHAPS), 200 μ M of each dATP, dGTP, dTTP, 100 μ M dCTP, 1 mCi α -(³²P)dCTP, 1 μ g of M13mp9 ssDNA annealed with 0.3 μ g M13 primer. Assays were performed with 2 and 3 μ l of enzyme in three different dilutions (final amount of enzyme 2.5 to 15 fmoles) yielding six reactions to calculate a mean value. As a reference *Pwo* DNA polymerase was used. The DNA/primer mix was prepared by heating 277.2 μ g M13mp9 ssDNA (Roche Molecular Biochemicals) and 156 μ g M13 sequencing primer (17mer forward primer, Roche Molecular Biochemicals) for 30 minutes to 55 °C and then cooling it for 30 minutes to room temperature.

Assay reactions were incubated for 30 minutes at 65 °C, stopped on ice by addition of 500 μ l of 10% TCA (4 °C) and kept on ice for another 10 minutes. Samples were filtered over GFC-filter (Whatman), filters washed three times with 5% TCA, dried and submitted to β -counting in 2 ml of scintillation fluid. One unit is defined as the amount of enzyme necessary to incorporate 10 nM dNTP into acid insoluble material at 65 °C in 30 minutes.

Example 3

Exonuclease Assays

Activity Assay

3 μ l (300 ng) of enzyme (approximately 5 Units of polymerase activity) were incubated with 5 μ g of 3H-labelled calf thymus DNA for 4 hours at 65 °C in a buffer containing 10 mM Tris-HCl/pH 8.9, 75 mM KCl, 1.5 MgCl₂, 10 mM CHAPS. Radioactivity liberated from calf thymus DNA was measured in a scintillation counter.

The assay used does not discriminate between the 3'-5' exonuclease activity and the 5'-3' exonuclease activity. 5'-3'-exonuclease activity has not been detected phenotypically or genotypically in B-type polymerases of *Thermococcales* (Perler, F. B., Kumar, S. and Kong, H. (1996) *Adv. Prot. Chem.*, 48, 377-435). Thus the values obtained can be regarded as 3'-5'-exonuclease activity.

In another assay, 1 μ g of molecular weight marker II (Roche Molecular Biochemicals) were incubated in same buffer as above with 5 U of the indicated protein with or without 200 μ M dNTP in a final volume of 50 μ l for 6 hours at 65 °C. The reaction products were separated by electrophoresis on 1% agarose gels.

3'-5' Exonuclease processivity assay

The previously described heparin trap method was used (Reddy, M. K., Weitzel, S. E. and von Hippel, P. H. (1992) *J. Biol. Chem.*, 267(20), 14157-14166; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). A reaction mix (10 μ l) containing 10 mM Tris-HCl/pH 8.9, 75 mM KCl, 10 mM CHAPS and 0.5 pmoles of a 5'-DIG-labeled 24mer oligonucleotide was prewarmed for 1 minute at 68 °C in a thermocycler. Unless otherwise noted, 1 pmol of the enzyme was preincubated for 1 minute at 68 °C with the substrate. The reaction was started by addition of MnCl₂ (final concentration: 4 mM) and heparin (final concentration: 1 mg/ml) to ensure single turnover conditions. After incubation for 4 minutes, the reaction was stopped by the addition of 5 μ l of formamide buffer (80% formamide, 10 mM EDTA, 1 mg/ml bromophenol blue, 1 mg/ml xylene xyanol). The efficiency of the heparin trap was checked in a control reaction by adding heparin and MnCl₂ prior to the addition of the enzyme. The samples were denatured for 3 minutes at 90 °C and subjected to denaturing gel electrophoresis on a 17.5 % polyacrylamide/8 M urea gel. Gels were blotted to a positively charged nylon membrane (Roche Molecular Biochemicals) and the blots developed with CPD-Star (Roche Molecular Biochemicals) according to the manufacturers instructions.

Example 4

lacI-based PCR fidelity assay

We used the *lacI*-based PCR fidelity assay described by Frey and Suppmann (Frey, M. and Suppmann, B. (1995) *Biochemica*, 2, 34-35). This method is based on the amplification, circularization and transformation of the pUC19 derivative pUCQ17, which contains a functional *lacI*^q allele (Barnes, W. M. (1994) *Proc. Natl. Acad. Sci. USA*, 91, 2216-2220). PCR-derived mutations in *lacI* result in a de-repression of the expression of *lacZ* α and subsequent formation of a functional β -galactosidase enzyme, which can be easily detected on X-Gal indicator plates.

The truncated *lacI* gene of pUC19 was substituted by a functional copy of *lacI*^q. A 178 bp *Pvu II*-*Afl III* fragment was replaced by a 1121 bp DNA fragment encoding *lacI*^q. The α -complementing *E. coli* strain DH5 α , once transformed with the resulting plasmid pUCIQ17 (3632 bp), produces white (*LACI*⁺) colonies on LB plates containing ampicillin (100 μ g/ml) and X-Gal (0,004% w/v). For the PCR, pUCIQ17 was linearized by digestion with *Dra II* and used as a template in an amount of 1 or 10 ng. Both primers have *Cla I* cleavage sites at their 5' ends. Oligonucleotide Cla33 (34mer, 24 matches: 5'-AGC TTA TCG ATG GCA CTT TTC GGG GAA ATG TGC G-3') and Oligonucleotide Cla55 (36mer, 26 matches: 5'-AGC TTA TCG ATA AGC GGA TGC CGG GAG CAG ACA AGC-3') resulted in a PCR product of 3493 bp.

The reactions were performed with 1 or 5 pmol of protein in the *Tag* polymerase PCR buffer described below or for the control reactions in the manufacturers PCR buffers with 2.5 U of enzyme. The cycle conditions were 10 sec denaturation at 94 °C, 30 sec annealing at 57 °C and 4 min elongation at 72 °C for 18, 24 or 30 cycles depending on the enzyme.

After PCR, the yield of amplification product was determined at (OD_{260nm} or in agarose gel) and the DNA fragments submitted to phenol/chloroform extraction to eliminate any protein. After digestion with *ClaI*, the DNA fragments were purified from a preparative agarose gel. Ligation reactions were carried out with the Rapid Ligation Kit (Roche Molecular Biochemicals), the reactions contained 30 ng DNA. The resulting circular plasmids were transformed in *E. coli* DH5 α as described by Hanahan (Hanahan, D. (1983) *J. Mol. Biol.*, 166, 557-580) and plated on LB Amp/X-Gal plates described above. After incubation overnight at 37 °C, blue and white colonies were counted. The error rate (f) per bp was calculated with a rearranged equation published by Keohavong and Thilly (Keohavong, P. and Thilly, W. G. (1989) *Proc. Natl. Acad. Sci. USA*, 86, 9253-9257): $f = -\ln F / d \times b$ bp.

Where F is the fraction of white colonies (white colonies/ total colonies); d is the number of DNA duplications: 2^d = output DNA/input DNA and b is the effective target size (1080 bp) of the *lacI* gene. There are 349 phenotypically identified (by colour screening) single-base substitutions (non-sense and mis-sense) at 179 codons (approximately 50% of the coding region) within the *lacI* gene. (Provost, G. S., Kretz, P. L., Hamner, R. T., Matthews, C. D., Rogers, B. J., Lundberg, K. S., Dyaico, M. J. and Short, J. M. (1993) *Mut. research*, 288, 133-149). Frameshift errors which may occur at every position in the 1080 bp open reading frame of *lacI*, are not taken into account because little information is available for the specific polymerases used in PCR systems except for *Taq* DNA polymerase.

Example 5

Polymerase Chain Reactions

PCR was performed in a buffer optimized for *Taq* DNA polymerase and its mutants: 10 mM Tris-HCl/pH 8.9, 75 mM KCl, 1.5 MgCl₂, 10 mM CHAPS, 200 μ M dNTP. 10 ng of λ DNA were used as a template and 30 pmol of each primer (20 bp, designed to yield the products of the desired length):

Lambda 1, universal forward primer: 5'-GAT GAG TTC GTG TCC GTA CAA CA-3',

Lambda 3.3: 5'-CTC ATC AGC AGA TCA TCT TCA GG-3',

Lambda 8: 5'-ACT CCA GCG TCT CAT CTT TAT GC-3',

Lambda 9: 5'-GAT GGT GAT CCT CTC TCG TTT GC-3'.

Lambda 3.3, 8 and 9 were used as reverse primers for the amplification of 3 kb, 3.5 kb and 7.5 kb fragments respectively.

Template, primers and nucleotides were prepared in mix 1 in a volume of 25 μ l. Then 25 μ l of mix 2 containing the buffer and enzyme (1 pmol *Taq* wild type or mutant; or 2.5 U control enzyme) were added. All reactions were prepared in duplicate. The amplification was performed in a 2400 GeneAmp thermocycler (Perkin Elmer). The cycle conditions were: 2 min at 94 °C, 10 cycles with 10 sec denaturation at 94 °C, 30 sec annealing at 58 °C and elongation at 72 °C. Elongation times depended on the length of the product (3 min for 3.3 kb, 4.3 min for 5 kb and 7 min for 7.5 kb). Another 20 cycles were performed with increasing the elongation times by 20 sec/cycle. The reaction was finished by 7 minutes at 72 °C. The tubes were kept at 4 °C until separation by electrophoresis on 1% agarose gels.

The improvement of the PCR performance of the mutants was also studied in a "time-dependent PCR". A 2 kb fragment was amplified from lambda DNA as described above. In these studies the

elongation time of the PCR was stepwise reduced (90 sec, 40 sec, 30 sec) to determine for each enzyme the minimal elongation time that was sufficient to amplify the 2 kb fragment. The following primers were used:

Lambda 1, universal forward primer: 5'-GAT GAG TTC GTG TCC GTA CAA CA-3',

Lambda 6, reverse primer: 5'-CTT CAT CAT CGA GAT AGC TGT CG-3'.

The temperature profile was as described above. The elongation times were kept constant over 30 cycles.

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Claims

1. A thermostable mutant B-type DNA polymerase having a Y-GG/A amino acid motif between the N-terminal 3'-5'-exonuclease domain and the C-terminal polymerase domain in the wild-type form of the polymerase whereas preferably the tyrosine of this motif is substituted in the mutant form of the polymerase and whereas this mutant DNA polymerase is suitable for polymerase chain reactions.
2. A mutant B-type DNA polymerase according to claim 1 having an amino acid with an aromatic side chain at the position of the tyrosine.
3. A mutant thermostable B-type DNA polymerase according to claim 1 having a Y→F, Y→W or Y→H mutation.
4. A mutant B-type DNA polymerase according to claim 1 having an amino acid with an hydrophilic side chain at the position of the tyrosine.
5. A mutant thermostable B-type DNA polymerase according to claim 1 having a Y→N or Y→S mutation.
6. A mutant thermostable B-type DNA polymerase according to claims 1-5 whereas the wild type form is obtainable from Euryarchaea.
7. A mutant thermostable B-type DNA polymerase according to claims 1-6 whereas the wild type form is obtainable from *Thermococcus aggregans*.
8. A mutant of a thermostable B-type DNA polymerase according to claims 1-6 whereas the amino acid sequence of the wild type form is $\geq 80\%$ homologue to the amino acid sequence of wild type *Tag* DNA polymerase.
9. A DNA encoding a thermostable mutant DNA polymerase according to claims 1-8.
10. A vector containing a DNA according to claim 9.

11. A transformed host cell comprising a vector according to claim 10.
12. A process for obtaining a polymerase according to claim 1-8 comprising the steps of cloning and mutagenesis of the gene, followed by the expression and purification of the protein.
13. Use of a polymerase according to claim 1-8 for synthesizing nucleic acids.
14. Use of a polymerase according to claims 1-8 for PCR reactions.

Abstract

Claimed are thermostable mutants of B-type DNA polymerases having a Y-GG/A amino acid motif between the N-terminal 3'-5'-exonuclease domain and the C-terminal polymerase domain whereas the tyrosine of the Y-GG/A amino acid motif is mutated and whereas these mutant DNA polymerases are suitable for PCR.

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Figure 1.

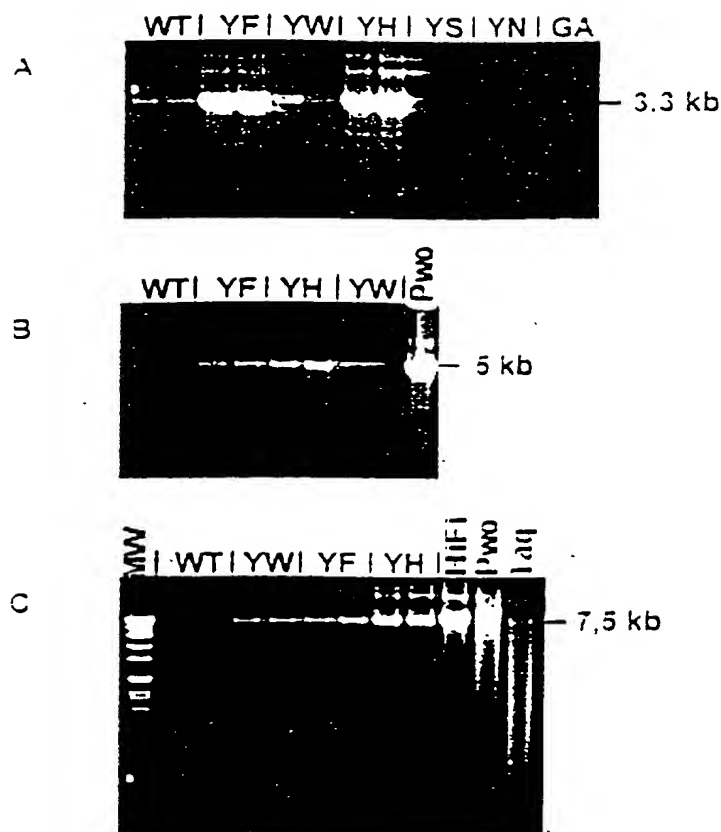
Pol activity and Exo activity in %

	WT	Y387F	Y387W	Y387H	Y387N	Y387S	G389A
Pol	100	160	92	93,6	6,4	17,8	10,7
Exo	100	90	71	98	205	187	236
Pol/Exo	1	1,77	1,29	0,96	0,03	0,09	0,04

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Figure 2



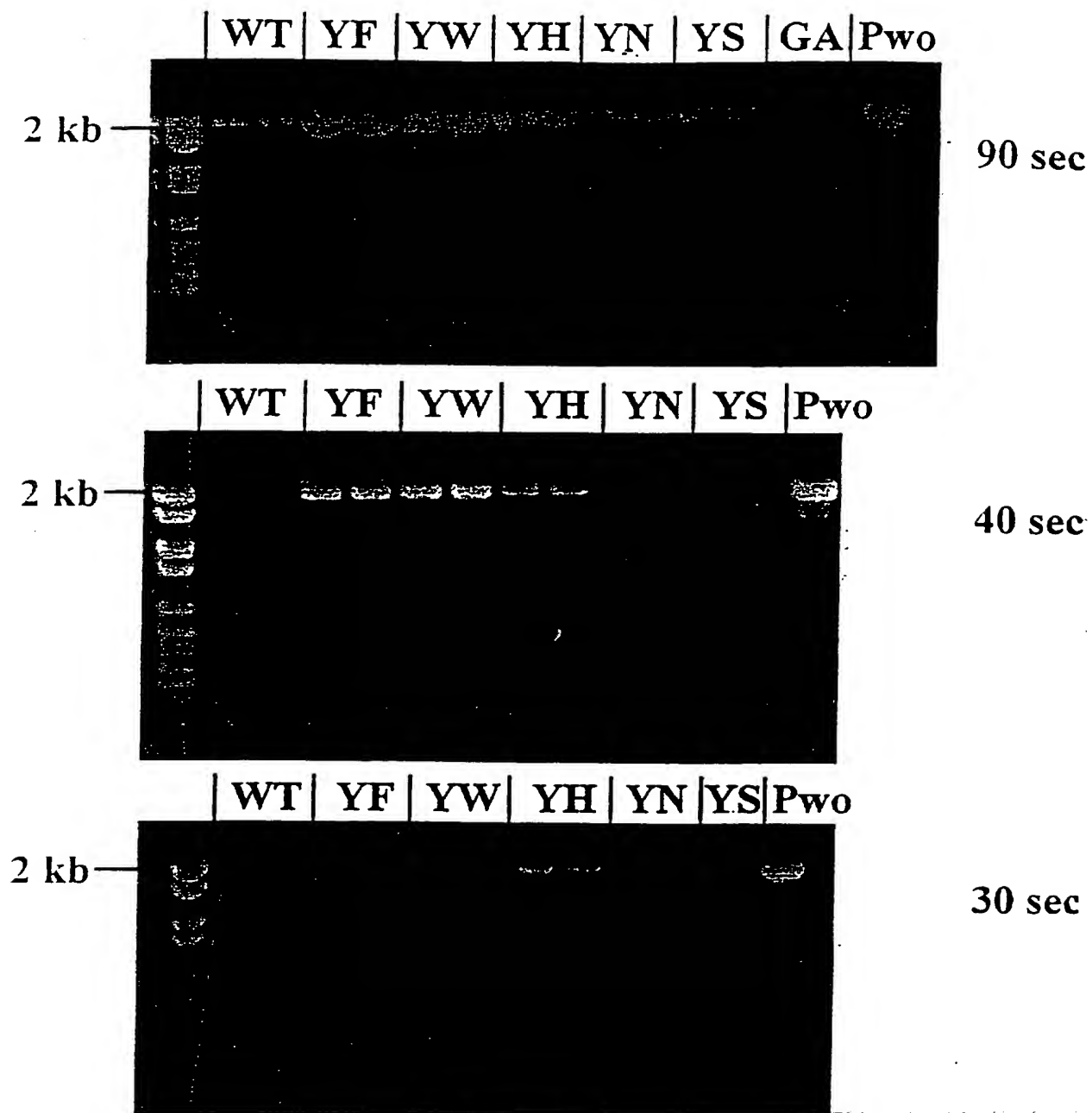


Figure 3

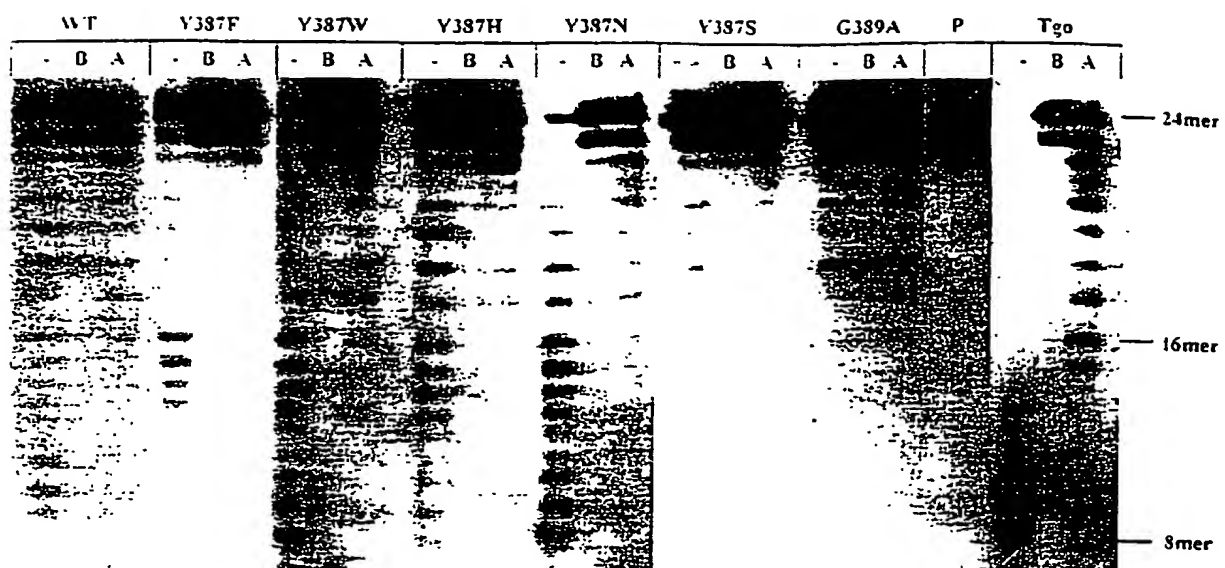


Figure 4

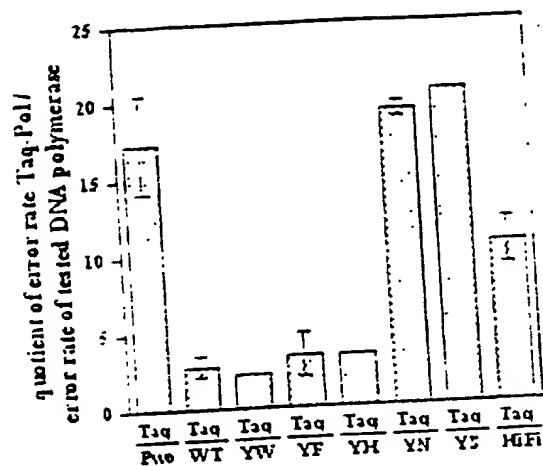
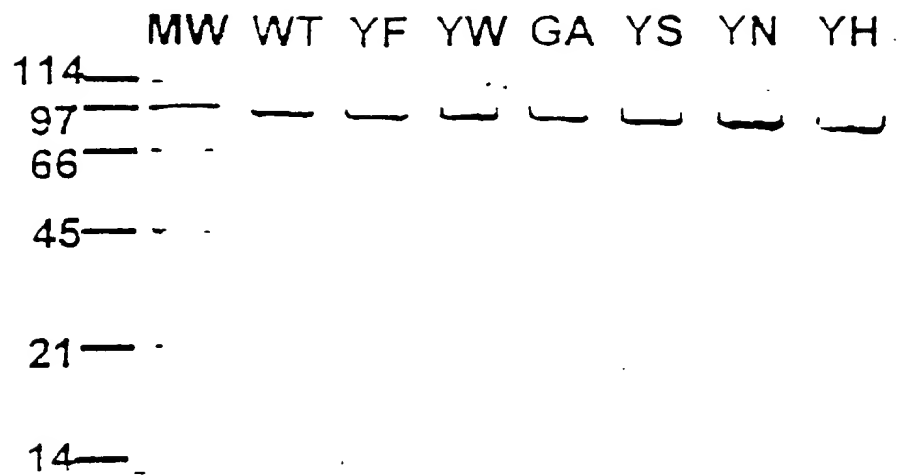
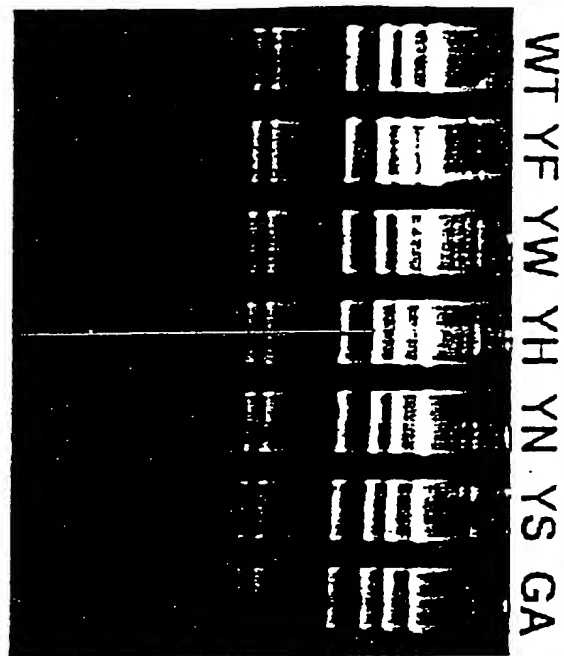


Figure 5

Figure 6



A



B

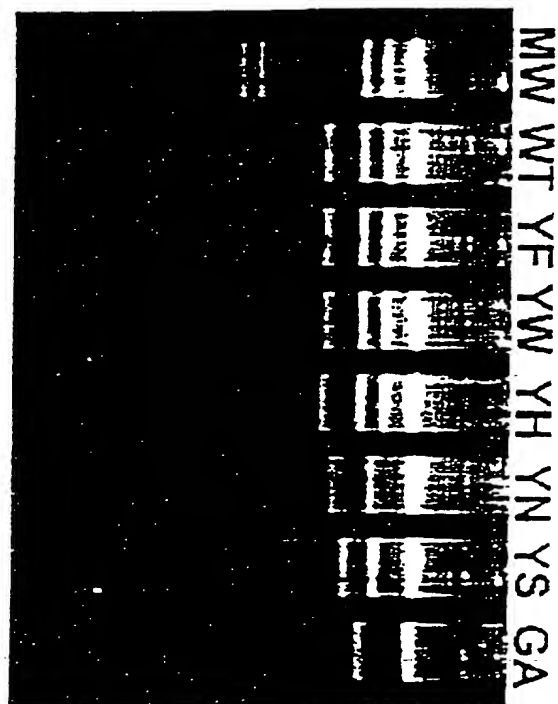


Figure 7

	E	R	R	R		G	(Y)	K	E	E		L	W	E	consensus									
aggregans	Y	R	R	R	L	T	T	L	G	G	Y	V	K	P	E	R	G	L	W	E	N			
litoralis	Y	K	R	R	L	R	T	T	L	G	G	Y	V	K	P	E	R	G	L	W	E	N		
umicodans	L	E	R	R	L	R	G	G	Y	A	G	G	Y	V	K	P	E	R	G	L	W	E	N	
spec. 9N7	L	A	R	R	L	R	G	G	Y	A	G	G	Y	V	K	P	E	R	G	L	W	E	N	
gorgonarius	L	A	R	R	L	R	G	S	Y	A	G	G	Y	V	K	P	E	R	G	L	W	E	N	
spec. KCO	L	A	R	R	L	R	Q	S	Y	E	G	G	Y	V	K	P	E	R	G	L	W	E	N	
abyssi	Y	E	R	R	L	R	G	S	Y	E	G	G	Y	V	K	P	E	R	G	L	W	E	N	
furiosus	Y	E	R	R	L	R	G	S	Y	E	T	G	G	F	V	K	P	E	R	G	L	W	E	N
honkoshii	Y	E	R	R	L	R	G	S	Y	E	G	G	Y	V	K	P	E	R	G	L	W	E	N	
M. jannaschii	Y	R	R	R	L	R	Y	E	G	G	Y	V	K	P	P	E	R	G	L	W	E	N		
M. oryzae	Y	R	R	R	L	R	Y	E	G	G	Y	V	K	P	P	E	R	G	L	W	E	N		
scitaticus	S	A	L	I	K	G	K	G	Y	K	G	A	V	I	D	P	P	A	G	I	T	T	N	
acidocalcarus	S	A	V	I	K	G	K	K	Y	K	G	A	V	I	D	P	P	A	G	V	Y	T	N	
slanicum	K	A	I	I	K	G	K	K	Y	A	G	A	V	I	D	P	P	L	G	I	T	T	N	
occultum	S	E	A	L	I	K	G	K	K	Y	Q	G	A	L	I	D	P	P	S	G	I	Y	T	N
cernix	V	G	A	I	I	K	D	K	K	Y	R	G	A	L	I	D	P	P	V	G	I	T	T	N
onwakueness	A	A	I	S	K	G	K	R	Y	K	G	A	V	I	D	P	P	A	G	V	P	T	N	

Figure 8

Figure 9/1

111
ATG ATA TTT GAC ACT GAC TAC ATA ACA AAG GAC GGT AAA GCG ATA ATT GCA ATT TTC AAG
Met Ile one asp thr asp tyr ile thr lys asp glv lys pro ile ile arg ile gne lys

112
AAA GAG AAC GCG GAA TTT AAA ATA GAA GTT GAT GCA CAT TTT GAG GCG TAC ATT TAC GGT
Lys glu asn gly glu gne lys ile glu leu asp pro his gne gln pro tyr ile tyr ala

113
TTT CTC AAA GAT GAC TCG GGT ATT GAT GAA ATA AAA GCA ATA AAA GCG GAG AGA GAC GCA
Leu leu lvs asp asp ser ala ile asp gln ile lvs ala ile lys gly glu arg his gly

114
AAA ATT CTC AGA GTA CTC GAT GCA GTC AAA GTT AAC AAG AAA TTT TTC GCG AGA GAT GTT
Lys ile val arg val val asp ala val lvs val lvs lvs lvs gne leu gly arg asp val

115
GAG CTC TCG AAG CTT ATA TTT GAG CAT GCG GAA GAC CTC GCG GCG CTA AGC GCG AAG ATA
Glu val thr lys leu ile gne glu his pro gln asp val pro ala leu arg gly lys ile

116
ACG GAA GAT GCA GGT CTC ATT GAC ATT TAT GAG TAC GAC ATA GCG TTT GCG AAG GCG TAC
arg glu his pro ala val ile asp ile thr glu thr asp ile pro gne ala lys arg tyr

117
CTC ATA GAG AAG GCG TTC ATC GGT ATG GAG GCG GAC GAG GAG GTT AAG GTA ATG GCG TTC
Leu Ile asp lvs gly leu ile pro met glu glu asp glu glu leu lys leu met ala gne

118
GAC ATT GAG ACG TTT TAC GAC GAG GGA GAC GAG TTT GCG AAG GCG GAG ATA ATA ATG ATA
asp ile glu thr gne thr his glu gly asp glu gne gly lys gly glu ile ile met ile

119
ACG TAC GCG GAT GAG GAA GAG GCA AGC GTA ATT ACA TCG AAG AAT ATT GAT CTC GCG TAC
ser tyr ala asp glu glu glu ala arg val ile thr asp lys asn ile asp leu pro tyr

120
GTT CAT GTT GTA TCG AAC GAA AGC GAG ATG ATA AAG GCG TTT CTC GAA ATT CTC AGC GAA
val asp val val ser asn glu arg glu met ile lys arg gne val gln ile val arg glu

121
AAA GAC GCG GAT CTC CTC ATA ACT TAC AAT GGA GAC AAC TTT GAT TTC GCG TAC CTT ATA
Lys asp pro asp val leu ile thr tyr asn gly asp asn gne asp leu pro tyr leu ile

122
AAA AGC GCA GAG AAG TTA GGA GTT ACT GTT CTC TTC GCG AGC GAC AAA GAA GAC GCG GAG
Lys arg ala glu lvs leu gly val thr leu leu leu gly arg asp lys glu his pro glu

123
GCG AAG ATT GAC AGA ATG GCG GAT AGC TTT GCG GTC GAA ATT AAA GCG AGA ATT GAC TTT
pro lys ile his arg met gly asp ser gne ala val glu ile lys gly arg ile his gne

124
GAT CTC TTC GCG GTT GTC GCG AGA ACC ATA AAC CTC GCA ACA TAC AGC CTT GAG GCA GTT
asp leu gne pro val val arg arg thr ile asn leu pro thr tyr thr leu glu ala val

125
TAT GAA GCG CTC TTC GGA AAA ACC AAA AGC AAG CTC GGT GCG GAG GAA ATC GCG GGT ATC
thr glu ala val leu gly lys thr lys ser lys leu gly ala glu glu ile ala ala ile

126
TTC GAA ACA GAG GAG ACC ATG AAG AAG CTC GCG GAG TAC TTC ATG GAA GAT GGT AGC GCA
trp glu thr glu glu ser met lys lys leu ala gln tyr ser met glu asp ala arg ala

127
GAT TAT GAA CTC GGA AAA GAG TTT TTC GCG ATG GAG GCA GAG CTA GCA AAG CTA ATA GCG
thr thr glu leu gly lys glu gne gne pro met glu ala glu leu ala lys leu ile gly

128
GAA AGC GTA TCG GAG CTC TCA AGA TCA AGC ACT GCG AAC GTT GTA GAG TCG TAC CTC TTA
gln ser val asp asp val ser arg ser ser thr gly asn leu val glu trp thr leu leu

Figure 9/2

1391/351

AGG GTG GCA TAT GAG AGG AAT GAG CTC GCT CCC AAC AAG CCC GAT GAA GAA GAG TAC AGA
arg val ala tyr glu arg asn glu leu ala pro asn lys pro asp glu glu glu tyr arg

1441/381

AGG GGT TTA AGG ACT ACT TAC CTC GGA GGA TAC GTA AAA GAG CCC GAA AGA GGC TTA TGG
arg arg leu arg thr thr tyr leu gly gly tyr val lys glu pro glu arg gly leu trp

1501/401

GAG AAC ATC AGC TAT TTA GAC TTT AGG TGC GTA TAC CCC TCA ATT ATA GTT ACC CAC AAC
glu asn ile thr tyr leu asp pro arg cys leu tyr pro ser ile ile val thr his asn

1551/421

ATG TGC GGT GAG ACT TTA GAA AGA GAA GGC TGC AAG AAT TAC CAT GTT CCC GCG ATA GTA
val ser pro asp thr leu glu arg glu gly cys lys asn thr asp val ala pro ile val

1621/441

GGT TAT AAG TTC TGC AAG GAT TTT CCC GGT TTC ATT GCA TGT ATA CTC GCG GAA TTA ATC
gly thr lys pro cys lys asp pro pro gly pro ile pro ser ile leu gly glu leu ile

1681/461

ACA ATG AGG GAA GAA ATA AAG AAG AAG ATG AAA GGT ACA ATT GAC GCA ATA GAA AAG AAA
thr met arg gin glu ile lys lys lys met lys ala thr ile asp pro ile glu lys lys

1741/481

ATG GTT CAT TAT AGG GAA AGA GGT GTT AAA TTC GAG GCA AAG AGC TAT TAC GGT TAT ATG
met leu asp thr arg gin arg ala val lys leu his ala asn ser thr tyr gly tyr met

1801/501

GGC TAT CCC AAG CCC AGG TGC TAC TGC AAG GAA TGT CCC GAA ACC GTT ACC CCC TGC GGA
gly thr pro lys ala arg thr tyr ser lys glu cys ala glu ser val thr ala trp gly

1861/521

AGG CAC TAC ATA GAA ATG ACC ATA AAA GAG ATA GAG GAG AAA TTT GGA TTT AAG GTG GTA
arg his thr ile glu met thr ile lys glu ile glu glu lys pro gly pro lys val leu

1921/541

TAT GCG GAG ACT GAT GGT TTT TAC GCG ACA ATA CCC GGA GAA AAA CCT GAA ACA ATC AAA
tyr ala asp thr asp gly pro cys ala thr ile pro gly glu lys pro glu thr ile lys

1981/561

AAG AAA GGT AAG GAA TTC TTA AAA TAC ATA AAC TTC AAA GTT CCC GGT CTC CTC GAG GTT
lys lys ala lys glu pro leu lys tyr ile asn ser lys leu pro gly leu leu glu leu

2041/581

GAG TAT GAG GGC TTT TAC TTC AGA GGA TTT TTC GTC GCA AAG AAG CCC TAC CCC GTT ATA
glu tyr glu gly pro tyr leu arg gly pro pro val ala lys lys arg tyr ala val ile

2101/601

GAC GAA GAA GGT AGG ATA ACC ACA AGG GGT CTC GAA GTT GTA AGG AGG GAC TGC AGC GAA
asp glu glu gly arg ile thr thr arg gly leu glu val val arg arg asp thr ser glu

2161/621

ATA GCG AAA GAG ACC CAG GGT AAA GTC TTC GAG GCA ACA GTT AAA GAA GAT AGT CTC GAA
ile ala lys glu thr gin ala lys val leu glu ala ile leu lys glu asp ser val glu

2221/641

AAA GGT CTC GAA ATC GTT AAG GAC GTT GTT GAG GAG ATA GCA AAA TAC GAA CTC CCC GTT
lys ala val glu ile val lys asp val val glu glu ile ala lys tyr gin val pro leu

2281/661

GAA AAG GTT GTT ATC CAC GAG CAG ATT ACC AAG GAT GTA AGT GAA TAC AAA GCG ATT GCG
glu lys leu val ile his glu gin ile thr lys asp leu ser glu tyr lys ala ile gly

2341/681

GCT CAT GTA GCA ATA GCA AAG AGG CTT GGT GCA AAG GCA ATA AAA GTG AGA CCC GCG ACC
pro his val ala ile ala lys arg leu ala ala lys gly ile lys val arg pro gly thr

2401/701

ATA ATA AGC TAT ATC CTC CTC AGG GGA AGC GGA AAG ATA AGT GAC AGG GTA ATT TTC GTT
ile ile ser tyr ile val leu arg gly ser gly lys ile ser asp arg val ile leu leu

Figure 9/3

1131, 721

TCA GAG TAT GAT CCG AAA AAA CAC AAG TAC GAC CCG GAC TAC TAC ATA GAA AAC CAA GTT
ser glu tyr asp pro lys lys his lys tyr asp pro asp tyr tyr leu glu asn glu val

1131, 741

CTG CCG CCG GTG GTT AGG ATC GTT GAA GCC TTC GCG TAC AGA AAA GAG GAC TTA AAA TAC
leu pro ala val leu arg ile leu glu ala pro glu tyr arg lys glu asp leu lys tyr

1131, 761

GAA AGC TCA AAA CAG GTT GGA GTG GAC GCG TCG GTT AAG AAG TCG
glu ser ser lys glu val gly leu asp ala asp leu lys lys met

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